

Amendments to the Specification

Please replace the title of the invention with the following amended title:

DNA MOLECULES ENCODING BETA CLAMP DNA REPLICATION
PROTEINS OF GRAM POSITIVE BACTERIA AND THEIR USE TO SCREEN FOR
CHEMICAL INHIBITORS

Please replace the paragraph at page 1, lines 4–108 with the following amended paragraph:

The present application is a national stage application under 35 U.S.C. 371 of PCT US00/020666, which is a continuation-in-part of U.S. Patent Application Serial No. 09/235,245 filed January 22, 1999, now abandoned, which claims benefit of U.S. Provisional Patent Application Serial No. 60/093,727 filed July 22, 1998, and U.S. Provisional Patent Application Serial No. 60/074,522 filed January 22, 1998, all of which are hereby incorporated by reference. The present application also claims benefit of U.S. Provisional Patent Application Serial No. 60/146,178 filed July 29, 1999, which is hereby incorporated by reference.

Please replace the paragraph at page 21, lines 25–28 with the following amended paragraph:

Figure 9 compares the homology between the polypeptide encoded by *dnaE* of *S. aureus* and other organisms. An alignment is shown for the amino acid sequence of the *S. aureus dnaE* product (SEQ. ID. No. 85) with the *dnaE* products (alpha subunits) of *E. coli* (SEQ. ID. No. 86) and *Salmonella typhimurium* (SEQ. ID. No. 87).

Please replace the paragraph at page 21, lines 29–32 with the following amended paragraph:

Figure 10 compares the homology between the N-terminal regions of the gamma/tau polypeptides of *S. aureus* (SEQ. ID. No. 88), *B. subtilis* (SEQ. ID. No. 89), and *E. coli* (SEQ. ID. No. 90). The conserved ATP site and the cystines forming the zinc finger are indicated above the sequence. The organisms used in the alignment were: *E. coli* (GenBank); and *B. subtilis*.

Please replace the paragraph at page 22, lines 1–3 with the following amended paragraph:

Figure 11 compares the homology between the DnaB polypeptide of *S. aureus* (SEQ. ID. No. 91) and other organisms. The organisms used in the alignment were: *E. coli* (GenBank) (SEQ. ID. No. 92); *B. subtilis* (SEQ. ID. No. 93); *Sal.Typ.*, (*Salmonella typhimurium*) (SEQ. ID. No. 94).

Please replace the paragraph at page 22, lines 4–9 with the following amended paragraph:

Figures 12A-B show the alignment of the delta subunit encoded by *holA* for *E. coli* (SEQ. ID. No. 95) and *B. subtilis* (SEQ. ID. No. 96) (Figure 12A) and for the delta subunit of *B. subtilis* (SEQ. ID. No. 96) and *S. pyogenes* (SEQ. ID. No. 97) (Figure 12B). Figure 12A shows ClustalW generated alignment of ~~*S. pyogenes*~~ *B. subtilis* (Gram positive) delta (SEQ. ID. No. 96) to *E. coli* (Gram negative) delta (SEQ. ID. No. 95). Figure 12B shows ClustalW generated alignment of *B. subtilis* (Gram positive) delta (SEQ. ID. No. 96) to *S. pyogenes* (Gram positive) delta (SEQ. ID. No. 97).

Please replace the abstract of the disclosure with the following amended abstract:

The present invention relates to ~~alpha-large, alpha-small, delta, delta prime, tau, beta, SSB, DnaG, and DnaB~~ protein-encoding genes from Gram positive bacterium, preferably ~~*Streptococcus* and *Staphylococcus*~~ bacterium. ~~The formation of functional polymerase as well as the use of such a polymerase in sequencing and amplification is also disclosed. The individual genes and proteins or polypeptides are useful in identification of compounds with antibiotic activity.~~ Expression systems and host cells containing these genes are also disclosed.